

**WE CLAIM:**

1. A composition comprising a protein in crystalline form wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 4.
2. A composition according to claim 1 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 4.
3. A composition according to claim 1 wherein the protein consists consecutively of residues of SEQ. ID No. 4.
4. A composition according to claim 1 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.
5. A composition according to claim 1 wherein the protein crystal has a crystal lattice in a P2<sub>1</sub> space group.
6. A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=79.9Å, b=56.9Å, c=95.2Å, α=90°, β=90.5°, and γ=90°.
7. A composition comprising a protein in crystalline form wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 5.
8. A composition according to claim 7 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.
9. A composition according to claim 7 wherein the protein consists consecutively of residues of SEQ. ID No. 5.
10. A composition according to claim 7 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.
11. A composition according to claim 7 wherein the protein crystal has a crystal lattice in a P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub> space group.

12. A composition according to claim 7 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of  $a=92.1\text{\AA}$ ,  $b=97.6\text{\AA}$ ,  $c=138.9\text{\AA}$ , and  $\alpha=\beta=\gamma=90^\circ$ .
13. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice in a  $P2_1$  space group.
14. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of  $a=79.9\text{\AA}$ ,  $b=56.9\text{\AA}$ ,  $c=95.2\text{\AA}$ ,  $\alpha=90^\circ$ ,  $\beta=90.5^\circ$ , and  $\gamma=90^\circ$ .
15. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice in a  $P2_12_12_1$  space group.
16. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of  $a=92.1\text{\AA}$ ,  $b=97.6\text{\AA}$ ,  $c=138.9\text{\AA}$ , and  $\alpha=\beta=\gamma=90^\circ$ .
17. A composition comprising a protein, wherein at least a portion of the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.
18. A method for forming a crystal of a protein comprising:  
forming a crystallization volume comprising: a precipitant solution and a protein wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 4; and  
storing the crystallization volume under conditions suitable for crystal formation of the protein.
19. A method according to claim 18 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 4.
20. A method according to claim 18 wherein at least a portion of the protein consists consecutively of residues of SEQ. ID No. 4.
21. A method according to claim 18 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

22. A method according to claim 18 wherein the protein crystal has a crystal lattice in a  $P2_1$  space group.
23. A method according to claim 18 wherein the protein crystal has a crystal lattice having unit cell dimensions,  $\pm 5\%$ , of  $a=79.9\text{\AA}$ ,  $b=56.9\text{\AA}$ ,  $c=95.2\text{\AA}$ ,  $\alpha=90^\circ$ ,  $\beta=90.5^\circ$ , and  $\gamma=90^\circ$ .
24. A method according to claim 18, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.
25. A method for forming a crystal of a protein comprising:  
forming a crystallization volume comprising: a precipitant solution and a protein wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 5; and  
storing the crystallization volume under conditions suitable for crystal formation of the protein.
26. A method according to claim 25 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.
27. A method according to claim 25 wherein at least a portion of the protein consists consecutively of residues of SEQ. ID No. 5.
28. A method according to claim 25 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.
29. A method according to claim 25 wherein the protein crystal has a crystal lattice in a  $P2_12_12_1$  space group.
30. A method according to claim 25 wherein the protein crystal has a crystal lattice having unit cell dimensions,  $\pm 5\%$ , of  $a=92.1\text{\AA}$ ,  $b=97.6\text{\AA}$ ,  $c=138.9\text{\AA}$ , and  $\alpha=\beta=\gamma=90^\circ$ .
31. A method according to claim 25, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

32. A composition comprising an isolated protein consisting of SEQ. ID No. 4.
33. A composition according to claim 32 where the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.
34. A composition comprising an isolated protein consisting of SEQ. ID No. 4.
35. A method of identifying an entity that associates with a protein comprising:  
taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 4; and  
performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.
36. A method according to claim 35 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 4.
37. A method according to claim 35 wherein the protein crystal has a crystal lattice in a  $P2_1$  space group.
38. A method according to claim 35 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of  $a=79.9\text{\AA}$ ,  $b=56.9\text{\AA}$ ,  $c=95.2\text{\AA}$ ,  $\alpha=90^\circ$ ,  $\beta=90.5^\circ$ , and  $\gamma=90^\circ$ .
39. A method according to claim 35, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.
40. A method according to claim 35, the method further comprising measuring an activity of the protein when contacted with the one or more entities
41. A method according to claim 35, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present

42. A method according to claim 35, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.
43. A composition according to claim 42 where the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.
44. A composition comprising an isolated protein consisting of SEQ. ID No. 5.
45. A method of identifying an entity that associates with a protein comprising:  
taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 5; and  
performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.
46. A method according to claim 45 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.
47. A method according to claim 45 wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 5.
48. A method according to claim 45 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.
49. A method according to claim 45, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.
50. A method according to claim 45, the method further comprising measuring an activity of the protein when contacted with the one or more entities

51. A method according to claim 45, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present

52. A method according to claim 45, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.